

Figure 1.

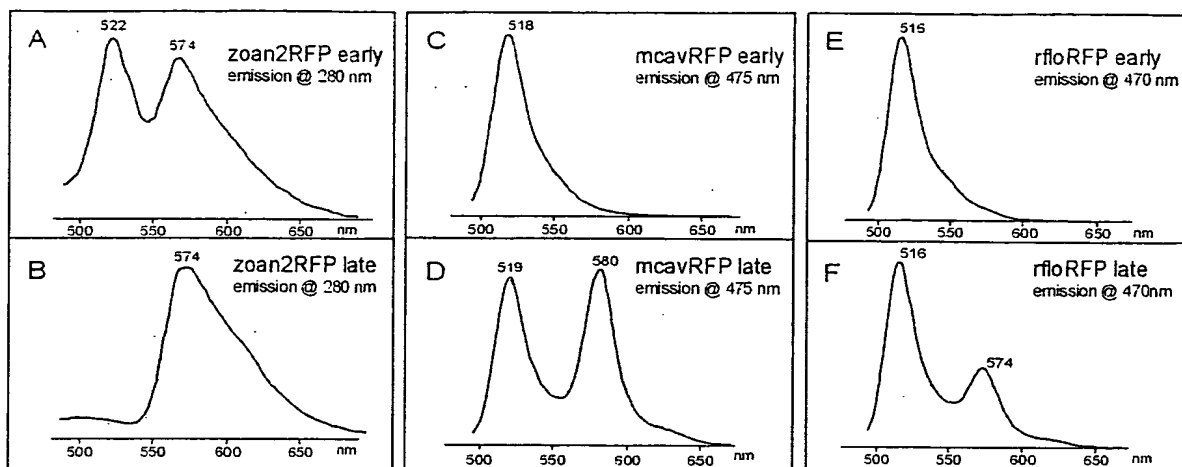


Figure 2.

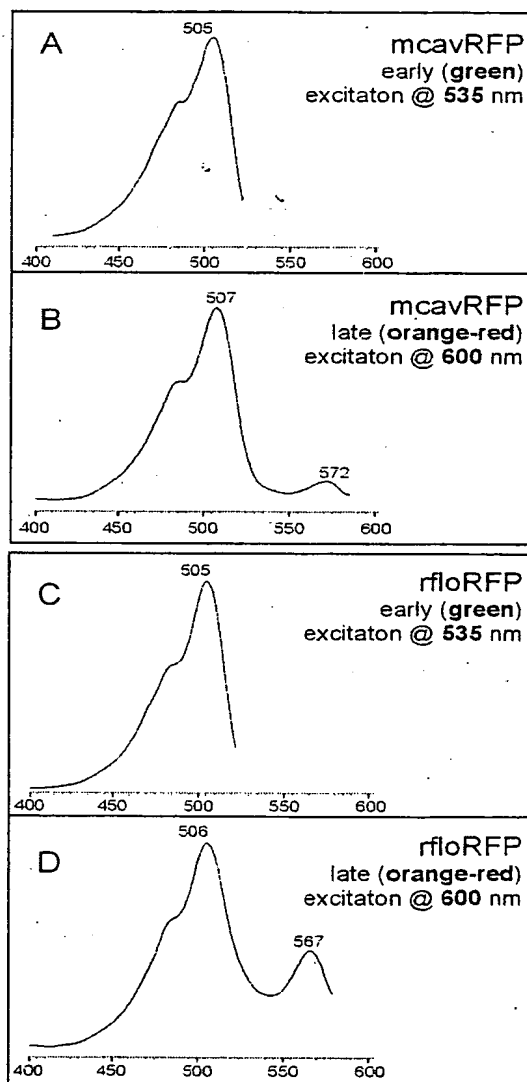


Figure 3.

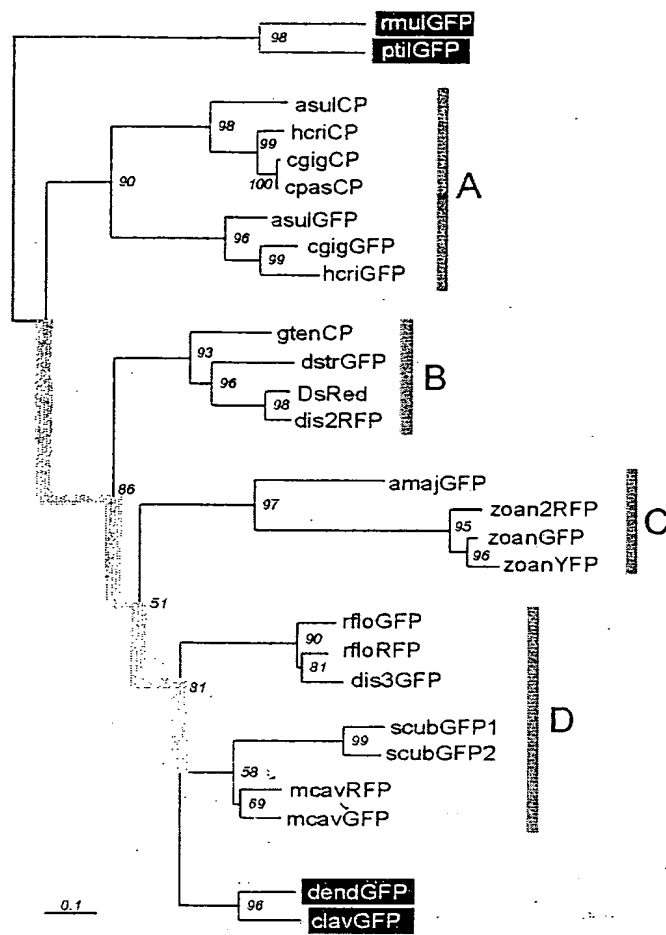


Figure 4

Protein ID (original ID)	GenBank accession #	Reference	Genus species (Class, Sub-class, Order)	Excitation maxima, nm	Emission maxima, nm	Representative spectra	color	Representative chromophore structure
anaGFP (amFP486)	AF168421	2	<i>Anemonia majano</i> (Anthozoa, Zoantharia, Actiniaria)	458	486		GREEN	
dsrGFP (dsFP483)	AF168420	2	<i>Discosoma striata</i> (Anthozoa, Zoantharia, Conallinophlaria)	456	484			
clayGFP (cFP484)	AF168424	2	<i>Clavularia</i> sp. (Anthozoa, Aleyonaria, Aleyonacea)	443	483			
GFP	M62653	34	<i>Aequorea victoria</i> (Hydrozoa, ... Hydroidea)	395, 471	508		YELLOW	?
cggGFP	AY037776	this paper	<i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria)	399, 482	486			
hcrGFP	AF420592	this paper	<i>Heteractis crispus</i> (Anthozoa, Zoantharia, Actiniaria)	405, 481	499			
ptGFP	AY015995	35	<i>Philosorvus</i> sp. (Anthozoa, Aleyonaria, Pennatulacea)	500	508		ORANGE-RED	DsRed:
rmuGFP	AY015996	35	<i>Renilla muelleri</i> (Anthozoa, Aleyonaria, Pennatulacea)	498	510			
zoaGFP (zFP506)	AF168422	2	<i>Zoanthus</i> sp. (Anthozoa, Zoantharia, Zoanthidea)	496	506			
asulGFP (asFP499)	AF322221	4	<i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria)	403, 480	499		PURPLE-BLUE	asulCP:
dis3GFP	AF420593	this paper	<i>Discosoma</i> sp.3 (Anthozoa, Zoantharia, Conallinophlaria)	503	512			
denGFP	AF420591	this paper	<i>Dendronephthya</i> sp. (Anthozoa, Aleyonacea)	494	508			
mcaVRFP	AY037769	this paper	<i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia)	506	516		absorbance only (asulCP)	?
rlcGFP	AY037772	this paper	<i>Ricordea florida</i> (Anthozoa, Zoantharia, Conallinophlaria)	508	517			
scubGFP1	AY037767	this paper	<i>Scophymia rubens</i> (Anthozoa, Zoantharia, Scleractinia)	497	506			
scubGFP2	AY037771	this paper	<i>Scophymia rubens</i> (Anthozoa, Zoantharia, Scleractinia)	497	506			
zoaNYFP (zFP538)	AF168423	2	<i>Zoanthus</i> sp. (Anthozoa, Zoantharia, Zoanthidea)	494, 528	538			
DsRed (dFP583)	AF168419	2	<i>Discosoma</i> sp.1 (Anthozoa, Zoantharia, Conallinophlaria)	558	583		?	?
dis2RFP (dsFP583)	AF272711	36	<i>Discosoma</i> sp.2 (Anthozoa, Zoantharia, Conallinophlaria)	573	693			
zoa2RFP	AY059642	this paper	<i>Zoanthus</i> sp.2 (Anthozoa, Zoantharia, Zoanthidea)	553	574			
mcaVRFP	AY037770	this paper	<i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia)	507, 572	519, 580		?	?
rlcRFP	AY037773	this paper	<i>Ricordea florida</i> (Anthozoa, Zoantharia, Conallinophlaria)	506, 567	516, 574			
asulCP (asCP)	AF246709	3, 4	<i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria)	568	none			
hcrCP (hcCP)	AF363776	5	<i>Heteractis crispus</i> (Anthozoa, Zoantharia, Actiniaria)	578	none		?	?
cggCP (cgCP)	AF363775	5	<i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria)	571	none			
cpasCP (cpCP)	AF363155	5	<i>Condylactis passiflora</i> (Anthozoa, Zoantharia, Actiniaria)	571	none			
glcCP (glCP)	AF363156	5	<i>Goniopora tenuidens</i> (Anthozoa, Zoantharia, Scleractinia)	580	none			

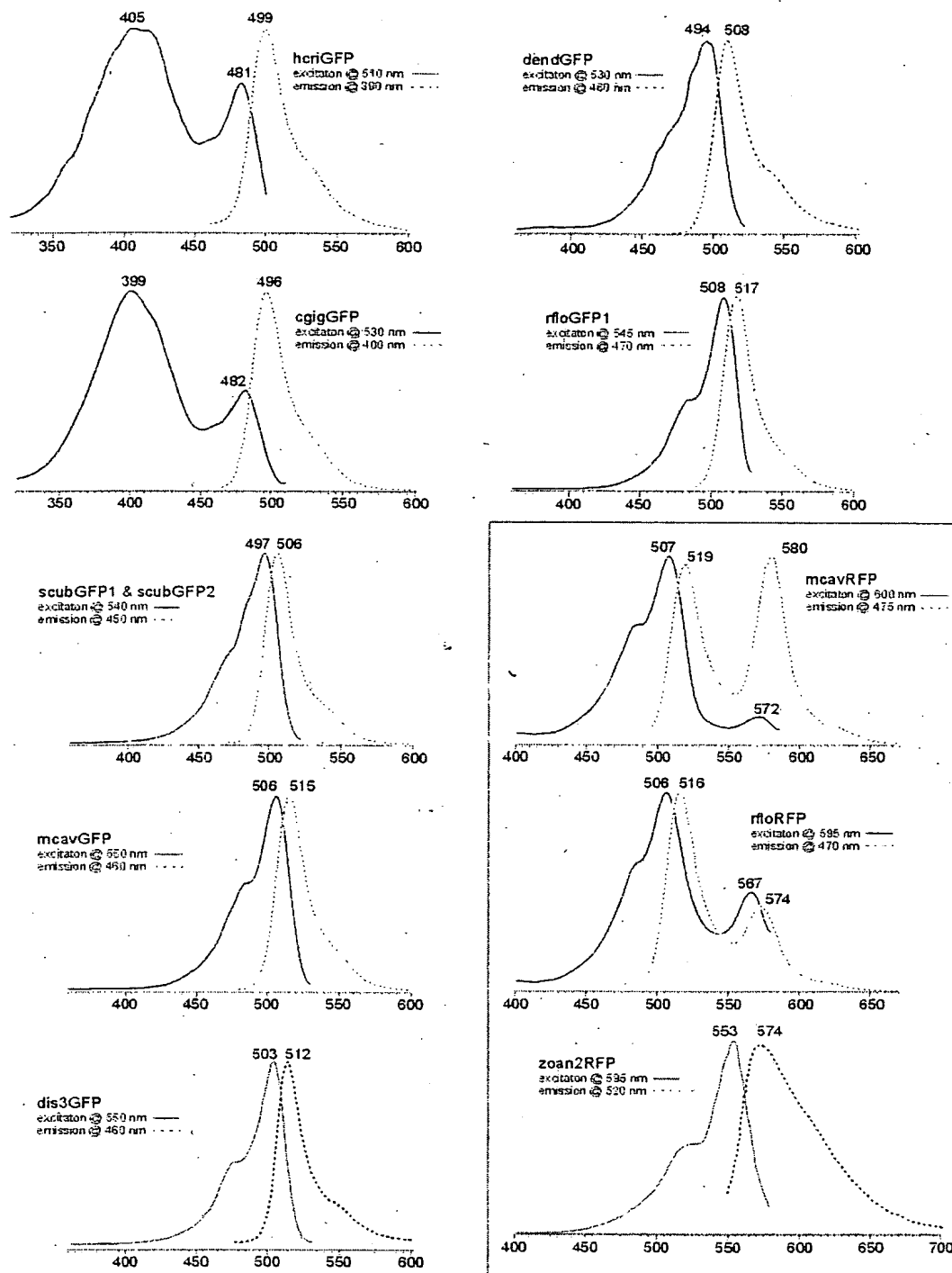
Table 1. Summary of spectral features and chromophore structures in the family of GFP-like proteins. Note that this paper uses different names for GFP-like proteins than proposed in original publications (the original names, where available, are given in brackets in the first column; see text for nomenclature details).

Figure 5

Table 2

clade	colors	Zoantharia orders
A	Green, purple-blue	Actiniaria
B	Green, orange-red, purple-blue	Corallimorpharia, Scleractinia
C	Green, yellow, orange-red	Actiniaria, Zoanthidea
D	Green, orange-red	Corallimorpharia, Scleractinia

Figure 6



10 20 30 40 50 60
 GFP : MSKGEELFTG-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 67
 cmulGFP : MSKQILKNTT-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 ptliGFP : MEIRNVLKNTT-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 asulCP : -HASF-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 hcr1CP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 cgigCP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 cpasCP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 asulGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 cgigGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 hcr1GFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 aasp7FP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 gtenCP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 dstrGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 DaRed : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 dis2RFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 amajGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 zoanGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 zoanYFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 zoan2RFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 rClorFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 rClorGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 dis3GFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 scubGFP1 : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 scubGFP2 : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 mcavRFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 mcavGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 dendGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 clavGFP : -HAGL-LS-VVFLDGLGQ-LEAFVSGSSEEDATYKLTLYFICTT-GKLV-PPVETTES- 71
 70 80 90 100 110 120 130 140 150 160
 GFP : VQCSRR-DRHKYK-SAM-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 cmulGFP : NNTTK-ND-S-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 ptliGFP : NNTTK-ND-S-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 asulCP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 hcr1CP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 cgigCP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 cpasCP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 asulGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 cgigGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 hcr1GFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 aasp7FP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 gtenCP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 dstrGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 DaRed : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 dis2RFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 amajGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 zoanGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 zoanYFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 zoan2RFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 rClorFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 rClorGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 dis3GFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 scubGFP1 : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 scubGFP2 : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 mcavRFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 mcavGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 dendGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 clavGFP : SNTIKVSG-P-DEEYV-ELIK-DOGHYKSRADVKEF-ELVNFRLKRLIKEDDNGHETMYNHNHNVY-MAQCKNGKLVKFKIRH- 169
 170 180 190 200 210 220 230
 GFP : MLEGG-SVQLADHY-ONTIPSGS-PUL-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 cmulGFP : MLEGG-SVQLADHY-ONTIPSGS-PUL-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 ptliGFP : MLEGG-SVQLADHY-ONTIPSGS-PUL-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 asulCP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 hcr1CP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 cgigCP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 cpasCP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 asulGFP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 cgigGFP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 hcr1GFP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 aasp7FP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 gtenCP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 dstrGFP : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236
 DaRed : KCGSG-RHLTCHLY-SGSAVALR-MSASTOSALSKEPNEKRDHMLLE-VTLAGITHGENDELYK- 236

FIGURE 8

Green fluorescent protein from *Heteractis crispa* hcriGFP

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      10      20      30      40      50      60
ATTTTGGACAGGTGTTCAACCAAGCAAATTTAAGAAGTCATCATCTTTATCTCAGTCAGG

      70      80      90     100     110     120
AAAATGTGTTCTTACATCAAAGAAACCATGCAAAGTAAGGTTTACATGGAAGGAAAAGTT
M C S Y I K E T M Q S K V Y M E G K V

      130     140     150     160     170     180
AACGACCACAACTTCAAGTGCAGTGCAGAAAGGAGAAACCATACAAAGGCTCACAA
N D H N F K C T A E G K G E P Y K G S Q

      190     200     210     220     230     240
AGCCTGACGATCACCGTAAGTGAAGGAGGTCTCTGCCATTTGCCTTCGACATTCTTTCA
S L T I T V T E G G P L P F A F D I L S

      250     260     270     280     290     300
CACGCCTTTTCGATATGGCAATAAGGTGTTGCGCAAGTACCCCAAAGATCATCCTGATTTT
H A F R Y G N K V F A K Y P K D H P D F

      310     320     330     340     350     360
TTTAAGCAGTCTCTTCCTGAAGGTTTTACTTGGGAAAGAGTAAGCAACTATGAGGACGGA
F K Q S L P E G F T W E R V S N Y E D G

      370     380     390     400     410     420
GGAGTCCTTACCGTTAAACAAGAACTAGTCTGGAGGGGAGATTGCATTATTTGCAAATTT
G V L T V K Q E T S L E G D C I I C K I

      430     440     450     460     470     480
AAAGCACATGGCACTAACTTCCCCGCAGATGGTCCGGTGATGCAAAAACGGACCAATGGA
K A H G T N F P A D G P V M Q K R T N G

      490     500     510     520     530     540
TGGGAGCCATCAACTGAAACGGTTATTCCACGGGGTGGAGGAATTCTGATGCGCGATGTG
W E P S T E T V I P R G G G I L M R D V

      550     560     570     580     590     600
CCCGCACTGAAGCTGCTTGGTAACAAAGGACATCTTCTCTGCGTCATGGAAACAACCTTAC
P A L K L L G N K G H L L C V M E T T Y

      610     620     630     640     650     660
AAGTCAAAAAAAAAAGGTGAACCTGCCAAACCGCACTTTTCATCATTTGAGAATGGAGAAG
K S K K K G E P A K P H F H H L R M E K

      670     680     690     700     710     720
GATAGTGTTAGTGACGATGAGAAGACCATTGAGCAGCACGAGAATGTGAGGGCAAGCTAC
D S V S D D E K T I E Q H E N V R A S Y

      730     740     750     760     770     780
TTCAATGATAGTGGAATGATCATTTTCCTTATTGATTTCAATGTTAGGGCATTTCAGTTT
F N D S G K *

      790     800     810     820     830     840
CCAAATTTTCTTAGACACAGTCTTTTCCTTTAGCTTCGTAGCCTACTTACCCATGTTTTG

      850     860
TTGAAGTCAATAAATAGCTAAGCACTAC (SEQ ID NOS: 01 & 02)
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Figure 9

Green fluorescent protein from *Dendronephthya* sp. dendGFP

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      10      20      30      40      50      60
5'CATATCGAGAAAGTTGTGAAACCAAATTCCTTACTCTACTTTTACTACCATGAATCTGATT
                                     M N L I

      70      80      90     100     110     120
AAAGAAGATATGAGGGTTAAGGTGCATATGGAAGGGAATGTAAACGGGCATGCTTTTGTG
K E D M R V K V H M E G N V N G H A F V

     130     140     150     160     170     180
ATTGAAGGGGAAGGAAAAGGAAGGCCCTACGAAGGGACACAGACCTTGAACCTGACAGTG
I E G E G K G R P Y E G T Q T L N L T V

     190     200     210     220     230     240
AAAGAAGGCGCGCCTCTCCCATTTTCTTACGACATCTTGACAACAGCATTGCACTACGGA
K E G A P L P F S Y D I L T T A L H Y G

     250     260     270     280     290     300
AACAGAGTATTCCTGAATACCCAGCAGATATCACGGATTATTTCAAGCAATCATTTTCT
N R V F T E Y P A D I T D Y F K Q S F P

     310     320     330     340     350     360
GAAGGATATTCCTGGGAAAGAACCATGACTTATGAAGACAAGGGCATTGTACCATCAGA
E G Y S W E R T M T Y E D K G I C T I R

     370     380     390     400     410     420
AGCGACATAAGCTTGGAAGGTGACTGCTTTTCCAAAACATTCGTTTTAATGGGATGAAC
S D I S L E G D C F F Q N I R F N G M N

     430     440     450     460     470     480
TTTCCCCCAAATGGTCCAGTTATGCAGAAGAAAACTTTGAAGTGGAACCATCCACAGAG
F P P N G P V M Q K K T L K W E P S T E

     490     500     510     520     530     540
AAGCTGCACGTGCGTGATGGGTTGCTTGTCGGTAATATTAACATGGCTCTGCTGCTTGAA
K L H V R D G L L V G N I N M A L L L E

     550     560     570     580     590     600
GGAGGTGGACATTACCTGTGTGACTTCAAACTACTTACAAAGCGAAGAAGGTTGTTTCAG
G G G H Y L C D F K T T Y K A K K V V Q

     610     620     630     640     650     660
TTGCCAGATTATCATTTTGTGGACCATCGCATTGAGATCTTGAGTAATGACAGCGATTAC
L P D Y H F V D H R I E I L S N D S D Y

     670     680     690     700     710     720
AACAAAGTGAAGCTGTACGAGCATGGGGTTGCTCGCTATTCTCCGTTGCCCAAGTCAGGC
N K V K L Y E H G V A R Y S P L P K S G

     730     740     750     760     770     780
CTGGTAGAGGTTCAAGGGAAAGCCATAATGACTGCATAGATAAACATGTAGTGAAGACCA
L V E V Q G K A I M T A *

     790     800     810     820     830     840
CATACTCGGGATTAGAGTTTAGGGATTGGTAGTTGTGGTAGATTCTAGCCTACAAATTTT

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TTGGG 3' (SEQ ID NO:03 & 04)

Figure 10

Red fluorescent protein from *Zoanthus* sp. zoanRFP

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      10      20      30      40      50      60
GAGTTGAGTTCTCGACTTCAGTTGTATCACTTTTGACGTATCAAGTGATCTATTCTCAAC

      70      80      90     100     110     120
ATGGCCCATTCAAAGCACGGACTAACAGATGACATGACAATGCATTTCCGTATGGAAGGG
M A H S K H G L T D D M T M H F R M E G

     130     140     150     160     170     180
TGCGTCGATGGACATAAGTTTGTAAATCGAGGGCAACGGCAATGGAAATCCTTTCAAAGGG
C V D G H K F V I E G N G N G N P F K G

     190     200     210     220     230     240
AAACAGTTTATTAATCTGTGTGTGATTGAAGGAGGACCACTGCCATTCTCCGAAGACATA
K Q F I N L C V I E G G P L P F S E D I

     250     260     270     280     290     300
TTGTCTGCTGCGTTTGACTACGGAAACAGGCTCTTCACTGAATATCCTGAAGGCATAGTT
L S A A F D Y G N R L F T E Y P E G I V

     310     320     330     340     350     360
GACTATTTCAAGAACTCGTGTCTGCTGGATATACGTGGCACAGGTCTTTTCGCTTTGAA
D Y F K N S C P A G Y T W H R S F R F E

     370     380     390     400     410     420
GATGGAGCAGTTTGCATATGCAGTGCAGATATAACAGTAAATGTTAGGGAAAACCTGCATT
D G A V C I C S A D I T V N V R E N C I

     430     440     450     460     470     480
TATCATGAGTCCACGTTTTATGGAGTGAACCTTTCCTGCTGATGGACCTGTGATGAAAAAG
Y H E S T F Y G V N F P A D G P V M K K

     490     500     510     520     530     540
ATGACAATAATTGGGAACCGTCCTGCGAGAAAATCATACCAATAAATAGTCAGAAGATA
M T T N W E P S C E K I I P I N S Q K I

     550     560     570     580     590     600
TTAAAAGGGGATGTCTCCATGTACCTCCTTCTGAAGGATGGTGGGCGTTACCGCTGCCAG
L K G D V S M Y L L L K D G G R Y R C Q

     610     620     630     640     650     660
TTTGACACAATTTACAAAGCAAAGACTGAGCCAAAAGAAATGCCGGACTGGCACTTCATC
F D T I Y K A K T E P K E M P D W H F I

     670     680     690     700     710     720
CAGCATAAGCTCAACCGTGAAGACCGCAGCGATGCTAAGAATCAGAAATGGCAACTGATA
Q H K L N R E D R S D A K N Q K W Q L I

     730     740     750     760     770     780
GAACATGCTATTGCATCCCGATCTGCTTTACCCTGATAACAAAGGAGTTGCTATTGCATG
E H A I A S R S A L P *

     790     800     810     820     830     840
TGCATGCCTATTACGCTGATAAAAATGTAGTTTAAACATGCAATTGTATGTGCATGCACA

     850
TTACCCTGATA

```

(SEQ ID NOS:05 & 06)

Figure 11

Green fluorescent protein from *Scolymia cubensis* scubGFP1 (AY037767)

```

      10      20      30      40      50      60
5'TGTGACATTCAGTCATATAGGAGCCTCTATCGGAGCTGAGGTCCCATTACCGTTGTGAT
      70      80      90     100     110     120
TTGGACGGGAGCAGATCGAGAACAACMAGGGCTGTACGAGTCTGATAATTACTTTACAT
      130     140     150     160     170     180
CTACCAACATGCAGCGTGTGGGATGAAGGTTAAGGAACATATGAAGATCAAACGCGTA
      M Q R A G M K V K E H M K I K L R M

      190     200     210     220     230     240
TGGGAGGTACTGTAAACGGAAAGCATTTCGCGGTTAATGGGACAGGAGACGGCTACCCTT
      G G T V N G K H F A V N G T G D G Y P Y

      250     260     270     280     290     300
ATCAGGAAAACAGATTTTGAAACTTATCGTCAAGGCAGCGAACCTCTGCCTTTCGCTT
      Q G K Q I L K L I V E G S E P L P F A F

      310     320     330     340     350     360
TTGATATCTTGTGACGAGCATTCCAGTATGGCAACAGGGCATTACCCGAATACCCAACAG
      D I L S A A F Q Y G N R A F T E Y P T E

      370     380     390     400     410     420
AGATAGCAGACTATTTTCAAGCAGTCGTTTGTAGTTTGGCGAGGGGTTCTCCTGGGAACGAA
      I A D Y F K Q S F E F G E G F S W E R S

      430     440     450     460     470     480
GTTTCACTTTTCGAAGATGGGGCCATTTGCGTCGCCACCAACGATATAACGATGGTTGGTG
      F T F E D G A I C V A T N D I T M V G G

      490     500     510     520     530     540
GTGAGTTTCAGTATGATATTCGATTGTGATGGTCTGAACCTCCCTGAAGATGGTCCAGTGA
      E F Q Y D I R F D G L N F P E D G P V M

      550     560     570     580     590     600
TGCAAAAGAAAACCGTAAATGGGAGCCATCCACTGAGATAATGTATATGCAAAATGGAG
      Q K K T V K W E P S T E I M Y M Q N G V

      610     620     630     640     650     660
TGCTGAAGGGTGAGGTTAACATGGCTCTGTTGCTTCAAGACAAAAGCCATTACCGTTGCC
      L K G E V N M A L L L Q D K S H Y R C D

      670     680     690     700     710     720
ACCTCAAACTACTTACAAAGCTAAGAATAATGTGCCGCATCCTCCAGGCTACCACTATG
      L K T T Y K A K N N V P H P P G Y H Y V

      730     740     750     760     770     780
TGGATCACTGCATTGAAATACTCGAAGAACGTAAGGATCACGTTAAGCTGCGGGAGCATG
      D H C I E I L E E R K D H V K L R E H A

      790     800     810     820     830     840
CTAAAGCTCGTTCTAGCCTGTCACCTACCAGTGCAAAAGAACGAAAGGCTTAGGTGATAG
      K A R S S L S P T S A K E R K A *

      850     860     870     880     890     900
TCAAAAAGACAACAAGACGAAATGAAAGGTGTTTCATTGTTAGAAATTTGATATTTTCGAT
      910     920     930     940     950     960
TCAATGATTCGTTAAGGGATTGCTAGAGGCTAGCTAACAGGTTAACATCATAAGGATAG
      970     980     990    1000    1010    1020
AGATTTCGTTGCGGAGTTAGAACCTTATATTTCCGAATCCAMCTAGAGTCGTTGAGA
      1030    1040    1050    1060    1070    1080
AATTTATTAGAGACTAGCTTTAGAGTTACTTTTGTGAAAAAAGGTTTCCATTTTTCG
      1090    1100    1110    1120    1130    1140
GTTATTACAGCATTTAAAGCATAGGAATAGAGATTGCGTTATGGAAAATAACAGTAGGAA
      1150    1160    1170
AATACGTTGTGAAAAATAAAGTTGTTGTCGAAAAAATAA 3'

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(SEQ ID NOS:07&08)

FIGURE 12

Green fluorescent protein from *Scolymia cubensis* scubGFP2 (AY037771)

```

      10      20      30      40      50      60
5'CCTGGTGATTGGACGAGAGCAGATCGAGAATAGCAAGGTTTTACCAGCGTGATAATTTA
      70      80      90     100     110     120
CTTTACATCTAACAACTGCAATCTGCTGGGAAGAAGAATGTCGTTAAGGACTTCATGAA
      M Q S A G K K N V V K D F M K

      130     140     150     160     170     180
GATCACACTGCGTATGGACGGTGCTGTAAACGGGAAGCCCTTCGCGGTTAATGGAACAGG
      I T L R M D G A V N G K P F A V N G T G

      190     200     210     220     230     240
AGATGGCAACCCCTTATGGTGAATACAGAGTTTGAAGCTTACCGTCGATGGCAACAAACC
      D G N P Y G G I Q S L K L T V D G N K P

      250     260     270     280     290     300
TCTGCCTTTTGCTTTTGATATCTTGTGAGCAGCATTCAGTATGGCAACAGGGCATTAC
      L P F A F D I L S A A F Q Y G N R A F T

      310     320     330     340     350     360
CGAATACCCAAAAGAGATATCAGACTATTTCAAGCAGTCGTTGAGTTTGGCGAGGGGTT
      E Y P K E I S D Y F K Q S F E F G E G F

      370     380     390     400     410     420
TACCTGGGAACGAAGTTTCACTTTTGAAGACGGGGCCATTTGCGTCGCCACGAACGATAT
      T W E R S F T F E D G A I C V A T N D I

      430     440     450     460     470     480
AAAGATGGTTGGCGATGAGTTTCAATATAACATTCGATTGATGGTGTGAATTTCCCTGA
      K M V G D E F Q Y N I R F D G V N F P E

      490     500     510     520     530     540
AGATGGTCCWGTATGCAGAAGAAAACGGTGAAAGTGGGAGCCATCCACAGAGATAATGCG
      D G P V M Q K K T V K W E P S T E I M R

      550     560     570     580     590     600
TGTGCAAGGTGGAGTGCTAAAGGGTGAGGTTAATGCGCTCTGTTGCTTAAAGACAAAAG
      V Q G G V L K G E V N M A L L L K D K S

      610     620     630     640     650     660
CCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAATCCTGTCCCGCCGACGGC
      H Y R C D F K T T Y K A K N P V P P T A

      670     680     690     700     710     720
GCTTCCAGACTACCACTATGTGGATCACTGTATTGAAATCACCGAGGAAAATAGGGATTA
      L P D Y H Y V D H C I E I T E E N R D Y

      730     740     750     760     770     780
CGTTAAGCTGCAGGAGTATGCTAAAGCTCGTTCTGGCCTGCACCTGCCCCGAAGTGC AAA
      V K L Q E Y A K A R S G L H L P E L Q K

      790     800     810
GTAAAGGCTTAGGCGATAGTCAAGACGACAACGAGAAGA 3'

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(SEQ ID NO:09 & 10)

FIGURE 13

Red fluorescent protein from *Ricordea florida* rflorFP (AY037773)

```

      10      20      30      40      50      60
5'TGTGAAAGTTAACATTTTACTTTTACTTCTACCAGCATGAGTGCACCTCAAAGAGGAAATGA
      M S A L K E E M K

      70      80      90      100     110     120
AAATCAAGCTTACATTGGTGGGCGTTGTTAACGGGCACCCATTCAAGATCATTGGGGACG
      I K L T L V G V V N G H P F K I I G D G

      130     140     150     160     170     180
GAAAAGGCAAACCTATGAGGGATCGCAGGAATTAACCCCTTGCCGTGGTGAAGGAGGGC
      K G K P Y E G S Q E L T L A V V E G G P

      190     200     210     220     230     240
CTCTGCCCTTTCTCTTATGATATCCTGACAACGATAGTTCACTATGGCAACAGGGCATTG
      L P F S Y D I L T T I V H Y G N R A F V

      250     260     270     280     290     300
TGAATCCTCAAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCTGGTGCTG
      N Y P K D I P D I F K Q T C S G P G A G

      310     320     330     340     350     360
GATATTCCTGGCAAAGGACCATGAGTTTTGAAGACGGAGGCGTTTGCACTGCTACGAGCC
      Y S W Q R T M S F E D G G V C T A T S H

      370     380     390     400     410     420
ATATCAGGGTGGATGGCGACACTTTCAATTATGACATTCACCTTCATGGGAGCGGATTTC
      I R V D G D T F N Y D I H F M G A D F P

      430     440     450     460     470     480
CTCTTAATGGTCCAGTGATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATA
      L N G P V M Q K R T V K W E P S T E I M

      490     500     510     520     530     540
TGTTTCAATGTGATGGATTGCTGAGGGGTGATGTTGCCATGTCTCTGTTGCTGAAAGGAG
      F Q C D G L L R G D V A M S L L L K G G

      550     560     570     580     590     600
GCGGCGATTACCGATGTGACTTTAAACTATTTATAAACCCAAGAAGAATGTCAAGATGC
      G H Y R C D F K T I Y K P K K N V K M P

      610     620     630     640     650     660
CAGGTTACCATTTTGTGGACCACTGCATTGAGATAACGAGTCAACAGGACGATTACAACG
      G Y H F V D H C I E I T S Q Q D D Y N V

      670     680     690     700     710     720
TGGTTGAGCTGTACGAGGGTGCTGTAGCCCACTACTCTCTCTGCAGAAACCATGCCAAG
      V E L Y E G A V A H Y S P L Q K P C Q A

      730     740     750     760     770     780
CAAAGGCATAAAGCCAAACAACCCAAGAGGACAACAAGACATTTAATCAAATCACATCTT
      K A *

      790     800
TGTATTTTGGTTAGAGTTGAAAAAAA 3'

```

(SEQ ID NO:11 & 12)

FIGURE 14

Green fluorescent protein from *Ricordea florida* rfloGFP (AY037772)

```

      10      20      30      40      50      60
5'AGTCACCTCGGTGTTTTTAGGACAGGAAGGATCACGAGCAAGAGAAGAACTGTGAAAGTT
      70      80      90     100     110     120
AACACTTTACTCTACTTCTACCAGCATGAGTGCACCTCAAAGAGGAAATGAAAATCAAGCT
              M S A L K E E M K I K L

      130     140     150     160     170     180
TAAATGGTGGGCGTTGTTAACGGGCAGTCATTTAGATCGATGGGGAAGGAAAAGGCAA
      K M V G V V N G Q S F Q I D G E G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGAAATTAACCCCTGAAGTGGTGAAGGAGGGCCTCTGCTCTT
      P Y E G S Q K L T L E V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTTCAGTATGGCAACAGGGCATTCTGAACTACCC
      S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCTGATGGTGGATTTCCTG
      K D I P D I F K Q T C S G P D G G F S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAAGACGGAGGGGTTGCACTGCTTCAAACCATCAGCGT
      Q R T M T Y E D G G V C T A S N H I S V

      430     440     450     460     470     480
GGACGGCGACACTTTTTATTATGTGATAAGATTTAATGGAGAGAATTTCTCCAAATGG
      D G D T F Y Y V I R F N G E N F P P N G

      490     500     510     520     530     540
TCCAGTAATGCAGAAAAGACAGTGAAATGGGAGCCATCCACTGAGATAATGTTTGAACG
      P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGACATTGCCATGTCTCTGTTGCTGAAAGGAGGCGGCCATTA
      D G L L R G D I A M S L L L K G G G H Y

      610     620     630     640     650     660
CCGATGTGACTTTAAACTATTTATACACCCAAGAGGAAGGTCAACATGCCAGGTTACCA
      R C D F K T I Y T P K R K V N M P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATACAGAAGCAGACAAGGATTACAACATGGCTGTGCT
      F V D H C I E I Q K H D K D Y N M A V L

      730     740     750     760     770     780
CTCTGAGGATGCTGTAGCCCAACTCTCCTCTGGAGAAAAAAGCCAAGCAAAGGCGTA
      S E D A V A H N S P L E K K S Q A K A *

      790
AAGCCAAACAACCTAA 3'

```

(SEQ ID NO:13&14)

Figure 15

Red fluorescent protein from *Montastraea cavernosa* mcavRF? (AY037770)

```

      10      20      30      40      50      60
5'ACGCAGGGATTACCCCTGGTGATTTGGAAGAGAGACGACCGAGAACAACAAGAGCTGTAT
      70      80      90     100     110     120
AAGGCTGATATCTTACTTTACGTCTACCATCATGAGTGTGATTAAATCAGTCATGAAGAT
R L I S Y F T S T I M S V I K S V M K I

      130     140     150     160     170     180
CAAGCTGCGTATGGAAGGCAGTGTAACGGGCACAACCTTCGTAATTGTTGGAGAAGGAGA
K L R M E G S V N G H N F V I V G E G E

      190     200     210     220     230     240
AGGCAAGCCTTATGAGGGAACACAGAGTATGGACCTTACAGTCAAAGAAGGCGCACCTCT
G K P Y E G T Q S M D L T V K E G A P L

      250     260     270     280     290     300
GCCTTCGCCTACGATATCATGACAACAGTATTCCATTACGGCAATAGGGTATTCGCAA
P F A Y D I M T T V F H Y G N R V F A K

      310     320     330     340     350     360
ATACCCAAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGGAGTATTCCTGGGA
Y P K H I P D Y F K Q M F P E E Y S W E

      370     380     390     400     410     420
ACGAAGCATGAATTTGGAAGGCGGGGGCATTTCACCGCCAGGAACGAGATAACAATGGA
R S M N F E G G G I C T A R N E I T M E

      430     440     450     460     470     480
AGGCGACTGTTTTTTCAATAAAGTTCGATTTGATGGTGTGAACCTCCCCCCTAATGGTCC
G D C F F N K V R F D G V N F P P N G P

      490     500     510     520     530     540
AGTCATGCAGAAGAAGACGCTGAAATGGGAGCCATCCACTGAAAAATGTATGTGCGTGA
V M Q K K T L K W E F S T E K M Y V R D

      550     560     570     580     590     600
TGGAGTGTGACGGGTGATATCAACATGGCTTTGTTGCTTGAAGGAGGTGGCCATTACCG
G V L T G D I N M A L L L E G G S H Y R

      610     620     630     640     650     660
ATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGGGTGTCAAGTTACCAGATTATCA
C D F R T T Y R A K K K G V K L P D Y H

      670     680     690     700     710     720
CTTTGAGGATCACTCCATTGAGATTTTGCGCCATGACAAAGAATACACTGAGGTAAAGCT
F E D H S I E I L R H D K E Y T E V K L

      730     740     750     760     770     780
GTATGAGCATGCCGAAGCTCATTCTGGGCTGCCGAGGGTGGCAAAGTAAAGGCTTAACGA
Y E H A E A H S G L P R V A K *

      790
AAAGCCAAGACCACA 3'

```

(SEQ ID NO:15 & 16)

FIGURE 16

Green fluorescent protein from *Montastraea cavernosa* mcavGFP (AY037769)

```

      10      20      30      40      50      60
5'ATTCGCCCTGGTGATTTGGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA
      70      80      90     100     110     120
TCTTACTTACGCTTACCATCATGACAAGTGTTCACAGGAAAAGGGTGTGATTAACCAG
      M T S V A Q E K G V I K P D

      130     140     150     160     170     180
ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAACGGGCACAAGTTCGTGGTTGAAG
      M K M K L R M E G A V N G H K F V V E G

      190     200     210     220     230     240
GAGATGGAAAAGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG
      D G K G K P F D G T Q T M D L T V I E G

      250     260     270     280     290     300
GCGCACCATTCGCTTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG
      A P L P F A Y D I L T T V F D Y G N R V

      310     320     330     340     350     360
TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCTGAGGGGT
      F A K Y P E D I A D Y F K Q T F P E G Y

      370     380     390     400     410     420
ACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTCGATCGCCACAAACGACA
      F W E R S M T Y E D Q G I C I A T N D I

      430     440     450     460     470     480
TAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTGATGGTGTGA
      T M M E G V D D C F A Y K I R F D G V N

      490     500     510     520     530     540
ACTTTCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACTG
      F P A N G P V M Q R K T L K W E F S T E

      550     560     570     580     590     600
AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTG
      I M Y A R D G V L K G D V N M A L L L E

      610     620     630     640     650     660
AAGGAGGTGGCCATTACCGATGTGACTTCAAACACTACTTACAAAGCTAAGAAGGTTGTCC
      G G G H Y R C D F K T T Y K A K K V V R

      670     680     690     700     710     720
GGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT
      L P D Y H F V D H R I E I V S H D K D Y

      730     740     750     760     770     780
ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA
      N K V K L H E H A E A R H G L S R K A K

      790     800     810     820     830     840
AGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTTGTGA
      *

      850     860     870     880     890     900
AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTTCGATTCAAGGATTGTTCCG
      910     920     930     940     950     960
GGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTT
      970     980     990     1000    1010    1020
TGCGGGATTACAGCATGGGGATAGACTTTTAAACTCAGTTGTGGTCAAATGCAAGTAAG
      1030    1040    1050    1060
AAAACTGTAGTGAGAATAAACTTGTATCGAAGCCGAAAAA 3'

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(SEQ ID NOS: 17 & 18)

Figure 17

Green fluorescent protein from *Condylactis gigantea* cgigGFP (AY037776)

```

      10      20      30      40      50      60
5'ACAGCTGTTTCATCCACGCTCATTCAAGACGCCGTCAACTTTATTCCAGTCAGGAAAATGT
                                     M Y

      70      80      90     100     110     120
ATCCTTGGATCAAGGAAACCATGCGCAGTAAGGTTTACATGGAAGGAGATGTTAACAACC
P W I K E T M R S K V Y M E G D V N N H

     130     140     150     160     170     180
ACGCCTTCAAGTGCAGTGCAGTAGGAGAAGGAAAACCATACAAAGGCTCACAGACCTGA
A F K C T A V G E G K P Y K G S Q D L T

     190     200     210     220     230     240
CGATTACCGTCACTGAAGGAGGTCCTCTGCCATTTGCTTTTCGACATTCTTTACACGCCT
I T V T E G G P L P F A F D I L S H A F

     250     260     270     280     290     300
TTCAGTATGGCAACAAGGTGTTCCACCGATTACCCCGACGATATTCCTGATTTCTTTAAGC
Q Y G N K V F T D Y P D D I P D F F K Q

     310     320     330     340     350     360
AGTCTCTCTCGGATGGTTTTACTTGGAGAAGAGTAAGCACSTATGACGATGGAGGAGTCC
S L S D G F T W R R V S T Y D D G G V L

     370     380     390     400     410     420
TCACAGTTACCCAAGACACTAGTCTGAAGGAGATTGCATTATTTGCAACATTAAAGTCC
T V T Q D T S L K G D C I I C N I K V H

     430     440     450     460     470     480
ATGGCACTAACTTCCCCGAAAATGGTCCGGTGATGCAAAACAAGACCGATGGATGGGAGC
G T N F P E N G P V M Q N K T D G W E P

     490     500     510     520     530     540
CATCCAGCACTGAAACGGTTATTCCACAAGATGGAGGAATTGTTGCTGCGCGATCACCCG
S S T E T V I P Q D G G I V A A R S P A

     550     560     570     580     590     600
CACTAAGGCTGCGTGATAAAGGTCATCTTATCTGCCACATGGAAACAACCTTACAAGCCAA
L R L R D K G H L I C H M E T T Y K P N

     610     620     630     640     650     660
ACAAAGAGGTGAAGCTGCCAGAACTCCACTTTCATCATTTGCGAATGGAAAAGCTGAGTG
K E V K L P E L H F H H L R M E K L S V

     670     680     690     700     710     720
TTAGTGACGATGGGAAGACCATTAAAGCAGCACGAGTATGTGGTGGCTAGCTACTCCAAG
S D D G K T I K Q H E Y V V A S Y S K V

     730     740     750     760     770     780
TGCCTTCGAAGATAGGACGTCAATGATCATTTCCTTATTAATATCAATGATGTGGCTT
P S K I G R Q *

     790     800     810     820     830     840
TCAATTTTCCAAAATTTTGTTAAGACATAGGTCTTTTGGATTTTGGTAACCCCAACCTT
     850     860     870     880     890
AATTCCCAATAATTTTGTGGAAAGTCAAATAAAACCAGCCTTCCTGGGCCTTTAA 3'

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(SEQ ID NOS: 19 & 20)

FIGURE 18

Green fluorescent protein from *Agaricia fragilis* afraGFP (AY037765)

```

      10      20      30      40      50      60
5'CAAGGAAGCCAAATCTTTTACCAGAGATCTCGCGTGAAAGCAACCTATGAGTGATGGCGA
                                     M A I

      70      80      90     100     110     120
TTTCTACTCTAAAGAACGTATCATCATCGTTATTATATACTCCTGCAGCACTTGTGCTG
  S T L K N V I I I V I I Y S C S T C A V

     130     140     150     160     170     180
TTTGGTCAATTCAAACCTCTGAATCCTCTTTCACTAATGGGATTGCAGAGGAAATGAAGA
  W S N S N S E S S F T N G I A E E M K T

     190     200     210     220     230     240
CTAGGGTACATTTGGAGGGTACTGTAAACGGGCACCTCTTACAATTAAGGCGAAGGAA
  R V H L E G T V N G H S F T I K G E G R

     250     260     270     280     290     300
GAGGCTACCCTTACAAGGAGAACAGTTTATGAGCCTTGAGGTCGTCATGTTGCTCCTC
  G Y P Y K G E Q F M S L E V V N G A P L

     310     320     330     340     350     360
TGCCGTTCTCTTTTGATATCTTGACACCAGCATTTATGTATGGCAACAGAGTGTTCACCA
  P F S F D I L T P A F M Y G N R V F T K

     370     380     390     400     410     420
AGTACCCACCAACATACCAGACTATTTCAAGCAGACGTTTCTGAAGGGTATCACTGGG
  Y P P N I P D Y F K Q T F P E G Y H W E

     430     440     450     460     470     480
AAAGAAACATTCCTTTGAAGATCAGGCCGCGTGACGGTAACCAGCCACATAAGATTGG
  R N I P F E D Q A A C T V T S H I R L E

     490     500     510     520     530     540
AAGAGGAAGAGAGGCGTTTGTAAATAACGTCAGATTCACTGTGTGAACCTTTCCCCCTA
  E E E R R F V N N V R F H C V N F P P N

     550     560     570     580     590     600
ATGGTCCAGTCATGCAGAGGAGGATACTGAAATGGGAGCCATCCACTGAGAACATTTATC
  G P V M Q R R I L K W E P S T E N I Y P

     610     620     630     640     650     660
CGCGTGATGGGTTTCTGGAGGGCCATGTTGATATGACTCTTCGGGTTGAAGGAGGTGGCT
  R D G F L E G H V D M T L R V E G G G Y

     670     680     690     700     710     720
ATTACCGAGCTGAGTTCAAAAGTACTTACAAAGGGAAGACCCAGTCCGCGACATGCCAG
  Y R A E F K S T Y K G K T P V R D M P D

     730     740     750     760     770     780
ACTTTCATTTCATAGACCACCGCATTGAGATTACGGAGCATGACGAAGACTACACCAATG
  F H F I D H R I E I T E H D E D Y T N V

     790     800     810     820     830     840
TTGAGCTGCATGACGTATCCTGGGCTCGTTACTCTATGCTGCCGACTATGTAAGCGGAAA
  E L H D V S W A R Y S M L P T M

     850     860     870     880     890     900
AGGCAAGGCAACAAGACGCAAAACCGCCCTGTTGTCTCTTTTCATAAGAGATTGACAA
  910     920     930     940     950     960
CCGTGGTTCTTTGCCATTTAATTGAATTAGTTTAAATTAAATCTTTGGGATTGATGTAG
  970     980     990    1000    1010    1020
ACGCTTTGGTTGCTAAGTAAGAAAACATTTGTGATTATTAAATTTGTTGCCTGAAGCAAA
  1030
AAAAAAAAA 3'

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(SEQ ID NOS:21 & 22)

FIGURE 19

Green fluorescent protein from *Ricordea florida* rfloGFP2 (AY037774)

```

      10      20      30      40      50      60
5'AGCCACTTCGGTGTCTTGTGCGAGAGGAAGGATCACGAACAAGAGAAGAGCTGTAAAAGTT
      70      80      90     100     110     120
AAAATTTTACTTTACTTCTTCCAGCATGAATGCACTTCAAGAGGAAATGAAAATCAAGCT
      M N A L Q E E M K I K L

      130     140     150     160     170     180
TACAATGGTGGGCGTTGTTAACGGGCAGTCATTTAAGATCGATGGGAAAGGAAAAGGGAA
      T M V G V V N G Q S F K I D G K G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGGAATTGACCCTTAAAGTGGTGAAGGCGGGCCTCTGCTCTT
      P Y E G S Q E L T L K V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTTCAATATGGCAACAGGGCATTCGTGAACATACC
      S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAAACGTGTTCTGGTCTTGATGGCGGATATTCGTG
      K D I P D I F K Q T C S G L D G G Y S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAGGACGGAGGGGTTTGTACTGCTACAAGCAACGTCAGCGT
      Q R T M T Y E D G G V C T A T S N V S V

      430     440     450     460     470     480
GGTCGGCGACACTTTCAATTATGAAATTCACCTTTATGGGGGCGAATTTCTCTCAAATGG
      V G D T F N Y E I H F M G A N F P P N G

      490     500     510     520     530     540
TCCRGTTGATGCAGAAAAGAACAGTGAAGTGGGAGCCCTCCACTGAGATAATGTTTGAACG
      P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGATGTTCCCATGTCCTCTGTTGGCTGAAAGGAGGCGACCATTA
      D G L L R G D V P M S L L L K G G D H Y

      610     620     630     640     650     660
CCGATGTGACTTTTAAACTATTTTATAAACCAACAAGAAGGTCAAGCTGCCAGGTTACCA
      R C D F K T I Y K P N K K V K L P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATAAAGAGTCAAGAGAATGATTACAACATGGTTGCGCT
      F V D H C I E I K S Q E N D Y N M V A L

      730     740     750     760     770     780
CTTTGAGGATGCTGTAGCACACTACTCTCCTCTGGAGAAAAAGAGCCAGGCAAAGGCGTA
      F E D A V A H Y S P L E K K S Q A K A *

      790     800     810     820     830     840
AATCCAAACAACCTAAGAAGACGACAAGGCATTCAATCTAATCGCATGTTTGAATTTTGT
      850     860     870     880     890     900
GTTAGGAATGTGTTGGGTCAGACTAGGTCTAGAACGTTTCATTTTGGCTGGATTGTTTT
      910     920     930     940     950     960
ACTCAGTTATAGACAAGAAAAAATCTTAAATGACTTGGGTTGGATTGAGTTTCGGGCAC
      970     980     990    1000    1010    1020
TGTCATTCGGATTCTCTAGAAATATTTGAGACCAAGCCTTTTTTTGAGCTGAGAACGT

AATC 3'

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(SEQ ID NOS: 23 & 24)

FIGURE 20

Green fluorescent protein from *Montastraea cavernosa* mcavGFP2 (AY037768)

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      10      20      30      40      50      60
5'AGAGCTGTAGGGTGATATCTTACTTACGTCTACCATCATGACCAGTGTTCACAGGAAAA
      M T S V A Q E K

      70      80      90     100     110     120
GGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCA
      G V I K P D M K M K L R M E G A V N G H

      130     140     150     160     170     180
CAAGTTCGTGATTGAAGGAGATGGAAGGGAAGCCTTTCGACGGAACACAGACTATGGA
      K F V I E G D G K G K P F D G T Q T M D

      190     200     210     220     230     240
CCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGCTATCTTGACAACAGTATT
      L T V I E G A P L P F A Y A I L T T V F

      250     260     270     280     290     300
CGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCA
      D Y G N R V F A K Y P E D I A D Y F K Q

      310     320     330     340     350     360
GACATTTCTGAGGGGTACTTCTGGAACGAAGCATGACATACGAAGACCAGGGCATTTC
      T F P E G Y F W E R S M T Y E D Q G I C

      370     380     390     400     410     420
CATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAAAT
      I A T N D I T M M K G V D D C F V Y K I

      430     440     450     460     470     480
TCGATTTGATGGTGTGAACCTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAA
      R F D G V N F P A N G P V M Q R K T L K

      490     500     510     520     530     540
ATGGGAGCCATCCACTGAGAAAATGTATGCGCGTGATGGAGTGTGAAGGGTGATGTTAA
      W E P S T E K M Y A R D G V L K G D V N

      550     560     570     580     590     600
CATGGCTCTGTTGCTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAG
      M A L L L E G G G H Y R C D F K T T Y R

      610     620     630     640     650     660
AGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTGGACCATCGCATTGAGATTGT
      A K K V V Q L P D Y H F V D H R I E I V

      670     680     690     700     710     720
GAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGG
      S H D K D Y N K V K L Y E H A E A H S G

      730     740     750     760     770     780
GCTGCCGAGGCAGGCCAAGTAAAGGCTTAATGAAAAGCCAAGACGACAACAAGGAGAAAC
      L P R Q A K *

      790     800     810     820     830     840
AAAGTATTTTTTTGTTAAATTTCAAGGCATTTACTCGGAATTAGTATTTGATACTTTTCG
      850     860     870     880     890     900
ATTCAAGGATTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTTGTATTTTGTGAAAA
      910
AAAGATAGTTTCC 3'

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(SEQ.ID NOS: 25 & 26)

FIGURE 21

Green fluorescent protein homolog from *Montastraea annularis* mannFP (AY037766)

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      10      20      30      40      50      60
5'TGGTTAACGCAGAGTCGCGGGGGTTCCTGGCTAATAATTGATTCTATTTTGGGTGTGAC
      70      80      90     100     110     120
  ATTCAGGTTTAAAGCAGCATCCTCAGTGCTGAGGTCTCATTACCCTGGTGATTGGAAG
      130     140     150     160     170     180
  AGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAAAATCTTACTTGCCCTTACCACC
      190     200     210     220     230     240
  ATGAGTATGATTAAACCAGAAATGAAGATCAAGATGCGTATGGACGGTGCTGTAAACGGG
  M S M I K P E M K I K M R M D G A V N G

      250     260     270     280     290     300
  CACAAGTTCGTGATTACAGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAAACAGACTATG
  H K F V I T G E G S G E P F E G K Q T M

      310     320     330     340     350     360
  AACCTGACAGTCATAGACGGCGGACCTCTGCCTTTCGCTTTCGACATCTTGACAACAGCA
  N L T V I D G G P L P F A F D I L T T A

      370     380     390     400     410     420
  TTCGATTACGGCAMCAGGGTATTCGCCAAATACCCAGAAGACATCCAGACTATTTCAAG
  F D Y G X R V F A K Y P E D I P D Y F K

      430     440     450     460     470     480
  CAGTCGTTTCCTGAGGGGTTTCTTGGGAACGAAGCATGACTTACGAAGACGGGGGCATT
  Q S F P E G F S W E R S M T Y E D G G I

      490     500     510     520     530     540
  TGCATCGCCACAAATGACATAAAAAATGGAAGGCGACTGCTTTTCCTATGAAATTCGATT
  C I A T N D I K M E G D C F S Y E I R F

      550     560     570     580     590     600
  GATGGGGTGAACCTTTCCTGCCAATAGTCCAGTTATGCAGAAGAAGACCGTGAAATGGGAG
  D G V N F P A N S P V M Q K K T V K W E

      610     620     630     640     650     660
  CCATGCACCTGRGGAATGTATGTGCGTGATGGAGTGCTTAAAGGTGGTCTTAACATGGCT
  P C T X E M Y V R D G V L K G G L N M A

      670     680     690     700     710     720
  CTGTTGCTTGAAGGAGGTGGCCATTTCCGATGTGACTTGAAAACACTTACAAAGCTAAG
  L L L E G G G H F R C D L K T T Y K A K

      730     740     750     760     770     780
  AAGGTTGTCCAGATGCCAGACTATCACTTTGTGAATCACCGACTTGAGATAACATGGCAT
  K V V Q M P D Y H F V N H R L E I T W H

      790     800     810     820     830     840
  GACGAGGATTACAACAATGTTAAGCTGTCTGAGCATGCAGAAGCTCATTCTGGACTGCCA
  D E D Y N N V K L S E H A E A H S G L P

      850     860     870     880     890     900
  AGGCAGGCCAAATAAAGGCTTGACGAAAAGCCAAAACGGCAAAGAGTACAAGAAAGTATA
  R Q A K *

      910     920     930     940     950     960
  TATAAATGTATATTTTCAACTGAAAGGCATTCCACTCGGAATTAGTATTTGATACTTTC
      970     980     990     1000    1010    1020
  AATTCAAGGATTTATTTTGGGATTTGCTAGCCACTAGCTTTATTGTTAAATTAAGTTAAA
      1030    1040    1050    1060    1070    1080
  GACGGTTTAGCATTTTTCGGTATTACAACATAGGCACAGACGTCTTAACCCCAAGTAGTG
      1090    1100    1110    1120    1130
  GTCAGGTACAAGTAAGAAAACCTTGGTGAGAATAGACTTGTAGTCGAAAAAAA 3'

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(SEQ ID NOS:27 & 28)